

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 27, 2002, 03:36:38 : Search time 1259.04 Seconds

(without alignments)
7350.398 Million cell updates/sec

Title: US-09-893-615-88

Perfect score: 318
Sequence: 1 CAATATGTCCTCCAGTC.....GGACCAGCTGGAATATAGA 318Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapept 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

```

1: gb.ba:*
2: gb.htg:*
3: gb.in:*
4: gb.om:*
5: gb.ov:*
6: gb.pat:*
7: gb.ph:*
8: gb.pl:*
9: gb.pr:*
10: gb.ro:*
11: gb.sts:*
12: gb.sy:*
13: gb.un:*
14: gb.vi:*
15: em.ba:*
16: em.fun:*
17: em.hum:*
18: em.in:*
19: em.mu:*
20: em.om:*
21: em.or:*
22: em.ov:*
23: em.pat:*
24: em.ph:*
25: em.pl:*
26: em.ro:*
27: em.sts:*
28: em.un:*
29: em.vi:*
30: em.htg_hum:*
31: em.htg_inv:*
32: em.htg_other:*
33: em.htg_mus:*
34: em.htg_pin:*
35: em.htg_rtd:*
36: em.htg_vam:*
37: em.htg_vrt:*
38: em.sy:*
39: em.htgo_hum:*
40: em.htgo_mus:*
41: em.htgo_other:*

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	303.6	95.5	321	10	MMIG013
2	301.6	94.8	318	10	AF178620
3	301	94.7	318	10	AF178619
4	300.4	94.5	321	6	AR096128
5	300.4	94.5	321	6	AR210527
6	300.4	94.5	384	6	AR000010
7	300.4	94.5	384	6	AR060923
8	300.4	94.5	384	6	AR211055
9	300.4	94.5	384	6	AX032417
10	300.4	94.5	384	6	BD004717
11	300.4	94.5	9209	6	AR000007
12	300.4	94.5	9209	6	AR060920
13	300.4	94.5	9209	6	AR211052
14	300.4	94.5	9209	6	AX032414
15	300.4	94.5	9209	6	BD004714
16	300.4	94.5	18986	6	AR051652
17	300.4	94.5	18986	6	AR092290
18	298.8	94.0	384	6	AR015962
19	298.8	94.0	1370	10	MUSIGKAR
20	297.2	93.5	9209	6	AR015961
21	295.6	93.0	318	6	AR096196
22	295.6	93.0	318	6	AR210595
23	295.6	93.0	335	6	AR096195
24	295.6	93.0	335	6	AR210594
25	295.6	93.0	403	6	109200
26	295.6	93.0	403	10	MUSIGKCN
27	295.6	93.0	477	10	S76823
28	294.2	92.5	345	10	MUSIGKYA2A
29	294	92.0	403	6	105923
30	292.6	92.0	309	10	MMIGVKP4
31	292.4	91.9	302	10	MUSIGKAF
32	290.8	91.4	350	10	AY058906
33	290.8	91.4	384	10	MM005285
34	290.8	91.4	403	6	108812
35	290.8	91.4	732	6	A51863
36	290.8	91.4	732	6	A83237
37	290.8	91.4	732	6	AR085831
38	290.8	91.4	732	6	AR182961
39	289.4	91.0	318	12	AF277092
40	289.4	91.0	765	6	AX057984
41	289.4	91.0	1239	6	AX057945
42	289.4	91.0	1280	6	AX057947
43	288.2	90.6	435	6	A17967
44	288	90.6	360	10	AF029237
45	287.6	90.4	705	6	AR3197

ALIGNMENTS

```

RESULT 1
LOCUS      MMIG013
DEFINITION Mouse hyalidoma 2d3 mRNA for immunoglobulin kappa light chain V
region.
ACCESSION  X58586.Y00794
VERSION    X58586.1 GI:51562
KEYWORDS   Ig kappa light chain; Ig variable region; immunoglobulin.
SOURCE     Mus musculus.
ORGANISM   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 321)
AUTHORS   Week,K.
TITLE     Direct Submission

```

JOURNAL

Submitted (09-JAN-1989) K. Meek, University of Texas Southwestern Medical School, 5323 Harry Hines Blvd. Microbiology, Dallas Texas 75235, USA

REFERENCE

2 (bases 1 to 321)
Meek, K., Hasemann, C., Pollok, B., Alkan, S. S., Bratt, M., Sialoul, M., Uralin, J. and Capra, J. D.

AUTHORS

Structural characterization of antiidiotypic antibodies. Evidence that Ab2s are derived from the germline differently than Ab1s

JOURNAL

J. Exp. Med. 169 (2), 519-533 (1989)

MEDLINE

89094248

PUBMED

2492056

FEATURES

Location/Qualifiers

1..321

/organism="Mus musculus"

/strain="BALB/c"

/db_xref="taxon:10090"

/cell_line="Hybridoma 2D3-K"

1..321

/gene="Ig kappa light chain"

<1..>321

/gene="Ig kappa light chain"

/note="variable region"

/evidence="experimental"

<1..>321

/gene="Ig kappa light chain"

/note="variable region"

/codon_start=1

/product="Ig kappa light chain"

/protein_id="CAA41461.1"

/db_xref="GI:938245"

/translation="QIVLSQSPALISASPERVMTCRASSSVSYMHVYQKPGSSPK PMVATSNLASGVPARFSGSGSTSYSLTISRVEADATYYCHQMSSNPPTFGGTR LEIKR"

<1..>321

/gene="Ig kappa light chain"

/product="Ig kappa light chain"

/note="variable region"

BASE COUNT 78 a 92 c 80 g 71 t

ORIGIN

Query Match

Best Local Similarity 95.5%; Score 303.6; DB 10; Length 321;
Best Local Similarity 97.2%; Pred. No. 3.8e-90;

Matches

309; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db

1 CAATGTTCTCTCCAGTCTCCAGCAATCTCTGTCATCTCCAGGGAAGTCTACA 60

Db

1 CAATGTTCTCTCCAGTCTCCAGCAATCTCTGTCATCTCCAGGGAAGTCTACA 60

Db

1 CAATGTTCTCTCCAGTCTCCAGCAATCTCTGTCATCTCCAGGGAAGTCTACA 60

Db

1 CAATGTTCTCTCCAGTCTCCAGCAATCTCTGTCATCTCCAGGGAAGTCTACA 60

Db

1 CAATGTTCTCTCCAGTCTCCAGCAATCTCTGTCATCTCCAGGGAAGTCTACA 60

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1 CAATGTTCTCTCCAGTCTCCAGCAATCTCTGTCATCTCCAGGGAAGTCTACA 60

Db

1 CAATGTTCTCTCCAGTCTCCAGCAATCTCTGTCATCTCCAGGGAAGTCTACA 60

Db

1 CAATGTTCTCTCCAGTCTCCAGCAATCTCTGTCATCTCCAGGGAAGTCTACA 60

Accession

AF178620

AF178620.1 GI:5853223

KEYWORDS

Mus musculus.

Mus musculus.

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